

**PATENT APPLICATION**

**IN THE UNITED STATES PATENT AND TRADEMARK OFFICE**

In re application of

Yoji IKAWA et al.

Appln. No.: 09/670,568

Confirmation No.: Unassigned

Filed: September 27, 2000

For: HUMAN P51 GENES AND GENE PRODUCTS THEREOF

**RECEIVED**

MAY 25 2001

TECH CENTER 1600/2900

#101A  
KD  
5-30-01

Group Art Unit: 1642

Examiner: N. Davis

**RESPONSE TO NOTICE TO COMPLY WITH REQUIREMENTS FOR PATENT  
APPLICATIONS CONTAINING NUCLEOTIDE SEQUENCE AND/OR AMINO ACID  
SEQUENCE DISCLOSURES**

Assistant Commissioner for Patents  
Washington, D.C. 20231

Sir:

This response is in reference to the Notice to Comply, mailed April 27, 2001, issued in the above referenced patent application. As the Notice was mailed April 27, 2001, and set a one month period for response, this response is timely filed as it is being filed on or before May 27, 2001.

In the Notice, the Examiner states that the Sequence Listing previously submitted in this application fails to comply with the requirements of 37 C.F.R. §§1.821-1.825 for the reasons set forth in the attached Notice to Comply and Raw Sequence Listing Error Report.

The Error Report indicates that one line of amino acid sequence is missing from SEQ ID NO: 5. Applicants have corrected the error in the amended Sequence Listing submitted herewith.

**RESPONSE TO NOTICE TO COMPLY**

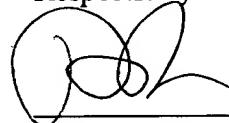
**Q61014**

In addition to the present Response to Notice to Comply, Applicants file herewith a paper copy and copy in computer readable form of the Sequencing Listing, a Statement to Support Filing and Submission in Accordance with 37 C.F.R. §§1.821-1.825, and a copy of the Notice.

Applicants assert that the Response to Notice to Comply and the enclosures are being timely filed, and that the enclosures bring the present application in full compliance with the requirements of 37 C.F.R. §§1.821-1.825.

Accordingly, Applicants respectfully request that the Examiner acknowledge that the Sequence Listing in the present application meets the requirements of 37 C.F.R. §§1.821-1.825.

Respectfully submitted,



Drew Hissong  
Registration No. 44,765

SUGHRUE, MION, ZINN,  
MACPEAK & SEAS, PLLC  
2100 Pennsylvania Avenue, N.W.  
Washington, D.C. 20037-3213  
Telephone: (202) 293-7060  
Facsimile: (202) 293-7860

Date: May 24, 2001

<b>Notice to Comply</b>	Application No.	Applicant(s)
	09/1670568	
	Examiner	Art Unit

**NOTICE TO COMPLY WITH REQUIREMENTS FOR PATENT APPLICATIONS  
CONTAINING NUCLEOTIDE SEQUENCE AND/OR AMINO ACID SEQUENCE  
DISCLOSURES**

Applicant must file the items indicated below within the time period set the Office action to which the Notice is attached to avoid abandonment under 35 U.S.C. § 133 (extensions of time may be obtained under the provisions of 37 CFR 1.136(a)).

The nucleotide and/or amino acid sequence disclosure contained in this application does not comply with the requirements for such a disclosure as set forth in 37 C.F.R. 1.821 - 1.825 for the following reason(s):

1. This application clearly fails to comply with the requirements of 37 C.F.R. 1.821-1.825. Applicant's attention is directed to the final rulemaking notice published at 55 FR 18230 (May 1, 1990), and 1114 OG 29 (May 15, 1990). If the effective filing date is on or after July 1, 1998, see the final rulemaking notice published at 63 FR 29620 (June 1, 1998) and 1211 OG 82 (June 23, 1998).

2. This application does not contain, as a separate part of the disclosure on paper copy, a "Sequence Listing" as required by 37 C.F.R. 1.821(c).

3. A copy of the "Sequence Listing" in computer readable form has not been submitted as required by 37 C.F.R. 1.821(e).

4. A copy of the "Sequence Listing" in computer readable form has been submitted. However, the content of the computer readable form does not comply with the requirements of 37 C.F.R. 1.822 and/or 1.823, as indicated on the attached copy of the marked -up "Raw Sequence Listing."

5. The computer readable form that has been filed with this application has been found to be damaged and/or unreadable as indicated on the attached CRF Diskette Problem Report. A Substitute computer readable form must be submitted as required by 37 C.F.R. 1.825(d).

6. The paper copy of the "Sequence Listing" is not the same as the computer readable from of the "Sequence Listing" as required by 37 C.F.R. 1.821(e).

7. Other:

**RECEIVED**

MAY 25 2001

**Applicant Must Provide:**

An initial or substitute computer readable form (CRF) copy of the "Sequence Listing" TECH CENTER 1600/2900

An initial or substitute paper copy of the "Sequence Listing", as well as an amendment directing its entry into the specification.

A statement that the content of the paper and computer readable copies are the same and, where applicable, include no new matter, as required by 37 C.F.R. 1.821(e) or 1.821(f) or 1.821(g) or 1.825(b) or 1.825(d).

For questions regarding compliance to these requirements, please contact:

For Rules Interpretation, call (703) 308-4216

For CRF Submission Help, call (703) 308-4212

PatentIn Software Program Support

Technical Assistance..... 703-287-0200

To Purchase PatentIn Software..... 703-306-2600

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IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

In re application of

Yoji IKAWA et al.

Appln. No.: 09/670,568

Confirmation No.: Unassigned

Group Art Unit: 1642

Filed: September 27, 2000

Examiner: N. Davis

For: HUMAN P51 GENES AND GENE PRODUCTS THEREOF

**STATEMENT TO SUPPORT FILING AND SUBMISSION IN  
ACCORDANCE WITH 37 C.F.R. §§ 1.821-1.825**

Assistant Commissioner for Patents  
Washington, D.C. 20231  
Box SEQUENCE

Sir:

In connection with a Sequence Listing submitted concurrently herewith, the undersigned hereby states that:

1. the submission, filed herewith in accordance with 37 C.F.R. § 1.821(g), does not include any new matter;
2. the content of the attached paper copy and the attached computer readable copy of the Sequence Listing, submitted in accordance with 37 C.F.R. § 1.821(c) and (e), respectively, are the same; and
3. all statements made herein of my own knowledge are true and that all statements made on information and belief are believed to be true, and further, that these statements were made with the knowledge that willful false statements and the like so made are punishable by



**STATEMENT TO SUPPORT FILING AND SUBMISSION  
IN ACCORDANCE WITH 37 C.F.R. §§ 1.821-1.825**

Q61014

fine or imprisonment, or both, under Section 1001 of Title 18 of the United States Code and that such willful false statements may jeopardize the validity of the application or any patent resulting therefrom.

Respectfully submitted,



Drew Hissong  
Registration No. 44,765

SUGHRUE, MION, ZINN,  
MACPEAK & SEAS, PLLC  
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Washington, D.C. 20037-3213  
Telephone: (202) 293-7060  
Facsimile: (202) 293-7860

Date: May 24, 2001

# RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/670,568

Source: 1642

Date Processed by STIC: 3/29/2001

**THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.  
PLEASE FORWARD THIS INFORMATION.**

FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:  
1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE  
APPLICANT, WITH A NOTICE TO COMPLY; or,  
2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A  
NOTICE TO COMPLY.  
FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION PLEASE CONTACT ROBERT WAX, 703-308-4216.  
PATENTIN 2.1 e-mail help: [patin21help@uspto.gov](mailto:patin21help@uspto.gov) or phone 703-306-4119 (R. Wax)  
PATENTIN 3.0 e-mail help: [patin3help@uspto.gov](mailto:patin3help@uspto.gov) or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER  
VERSION 3.0 PROGRAM ACCESSIBLE THROUGH THE U.S. PATENT AND  
TRADEMARK OFFICE WEBSITE SEE BELOW

Checker Version 3.0

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR 1.821-1.825 (effective October 1, 1990) (old rules) and the revised version (new rules) effective July 1, 1993 as well as World Intellectual Property Organization (WIPO) Standard ST 2.5. Checker Version 3.0 replaces the previous DOS-based version of Checker and is Y2K compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errors in sequence listings, thus saving time and money.

Checker Version 3.0 can be downloaded from the USPTO website at the following address:  
<http://www.uspto.gov/web/offices/pac/checker>

RAW SEQUENCE LISTING DATE: 03/29/2001  
PATENT APPLICATION: US/09/670,568 TIME: 10:20:49

Input Set : A:\sequence listing (p99-16).txt  
Output Set: N:\CRF3\03292001\I670568.raw

Does Not Comply  
Corrected Diskette Needed

APPLICANT: Ikawa, Yoji  
Otsuka Pharmaceutical Co. Ltd.  
TITLE OF INVENTION: Human p51 gene and its product  
FILE REFERENCE: P99-16  
CURRENT APPLICATION NUMBER:  
CURRENT FILING DATE: 2000-09-27  
PRIOR APPLICATION NUMBER: JP P1998-100467  
PRIOR FILING DATE: 1998-03-27  
NUMBER OF SEQ ID NOS: 23  
SOFTWARE: PatentIn Ver.2.0

## ERRORED SEQUENCES

389 <210> SEQ ID NO: 5  
 390 <211> LENGTH: 2270  
 391 <212> TYPE: DNA  
 392 <213> ORGANISM: Human  
 394 <220> FEATURE:  
 395 <221> NAME/KEY: CDS  
 396 <222> LOCATION: (145)..(2067)  
 398 <400> SEQUENCE: 5

399	tcgttcatat	caaagacagt	tgaaggaaat	gaattttgaa	acttcacgg	gtgccacc	60										
400	acagtactgc	cctgacc	ttt	acatccagcg	tttcgttagaa	acccagctca	tttcttgg	120									
401	aaagaaagtt	attaccgatc	cacc	atg	tcc	cag	agc	aca	cag	aca	aat	gaa	171				
402				Met	Ser	Gln	Ser	Thr	Gln	Thr	Asn	Glu					
403				1					5								
404	ttc	ctc	agt	cca	gag	gtt	ttc	cag	cat	atc	tgg	gat	ttt	ctg	gaa	cag	219
405	Phe	Leu	Ser	Pro	Glu	Val	Phe	Gln	His	Ile	Trp	Asp	Phe	Leu	Glu	Gln	
406	10						15				20					25	
407	cct	ata	tgt	tca	gtt	cag	ccc	att	gac	ttg	aac	ttt	gtg	gat	gaa	cca	267
408	Pro	Ile	Cys	Ser	Val	Gln	Pro	Ile	Asp	Leu	Asn	Phe	Val	Asp	Glu	Pro	
409							30				35				40		
410	tca	gaa	gat	ggt	gct	aca	aac	aag	att	gag	att	agc	atg	gac	tgt	atc	315
411	Ser	Glu	Asp	Gly	Ala	Thr	Asn	Lys	Ile	Glu	Ile	Ser	Met	Asp	Cys	Ile	
412							45				50				55		
413	cgc	atg	cag	gac	tcg	gac	ctg	agt	gac	ccc	atg	tgg	cca	cag	tac	acg	363
414	Arg	Met	Gln	Asp	Ser	Asp	Leu	Ser	Asp	Pro	Met	Trp	Pro	Gln	Tyr	Thr	
415							60				65				70		
416	aac	ctg	ggg	ctc	ctg	aac	agc	atg	gac	cag	cag	att	cag	aac	ggc	tcc	411
417	Asn	Leu	Gly	Leu	Leu	Asn	Ser	Met	Asp	Gln	Gln	Ile	Gln	Asn	Gly	Ser	
418							75				80				85		
419	tcg	tcc	acc	agt	ccc	tat	aac	aca	gac	cac	gct	cag	aac	agc	gtc	acg	459
420	Ser	Ser	Thr	Ser	Pro	Tyr	Asn	Thr	Asp	His	Ala	Gln	Asn	Ser	Val	Thr	
421							90				95				100		
422	gct	ccc	tcg	ccc	tac	gca	cag	ccc	agc	tcc	acc	ttc	gat	gct	ctc	tct	507
423	Ala	Pro	Ser	Pro	Tyr	Ala	Gln	Pro	Ser	Ser	Thr	Phe	Asp	Ala	Leu	Ser	

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424	110	115	120	
425	cca tca ccc gcc atc ccc tcc aac acc gac tac cca ggc ccg cac agt			555
426	Pro Ser Pro Ala Ile Pro Ser Asn Thr Asp Tyr Pro Gly Pro His Ser			
427	125	130	135	
428	tcc gac gtc tcc ttc cag cag tcg agc acc gcc aag tcc ggc acc tgg			603
429	Phe Asp Val Ser Phe Gln Gln Ser Ser Thr Ala Lys Ser Ala Thr Trp			
430	140	145	150	
431	acg tat tcc act gaa ctg aag aaa ctc tac tgc caa att gca aag aca			651
432	Thr Tyr Ser Thr Glu Leu Lys Lys Leu Tyr Cys Gln Ile Ala Lys Thr			
433	155	160	165	
434	tgc ccc atc cag atc aag gtc atg acc cca cct cct cag gga gct gtt			699
435	Cys Pro Ile Gln Ile Lys Val Met Thr Pro Pro Gln Gly Ala Val			
436	170	175	180	185
437	atc cgc gcc atg cct gtc tac aaa aaa gct gag cac gtc acg gag gtg			747
438	Ile Arg Ala Met Pro Val Tyr Lys Ala Glu His Val Thr Glu Val			
439	190	195	200	
440	gtg aag cgg tgc ccc aac cat gag ctg agc cgt gaa ttc aac gag gga			795
441	Val Lys Arg Cys Pro Asn His Glu Leu Ser Arg Glu Phe Asn Glu Gly			
442	205	210	215	
443	cag att gcc cct cct agt cat ttg att cga gta gag ggg aac agc cat			843
444	Gln Ile Ala Pro Pro Ser His Leu Ile Arg Val Glu Gly Asn Ser His			
445	220	225	230	
446	gcc cag tat gta gaa gat ccc atc aca gga aga cag agt gtc ctg gta			891
447	Ala Gln Tyr Val Glu Asp Pro Ile Thr Gly Arg Gln Ser Val Leu Val			
448	235	240	245	
449	cct tat gag cca ccc cag gtc act gaa ttc acg aca gtc ttg tac			939
450	Pro Tyr Glu Pro Pro Gln Val Gly Thr Glu Phe Thr Thr Val Leu Tyr			
451	250	255	260	265
452	aat ttc atg tgc aac agc agt tgc ggt ggg atg aac cgc cgt cca			987
453	Asn Phe Met Cys Asn Ser Ser Cys Val Gly Gly Met Asn Arg Arg Pro			
454	270	275	280	
455	att tta atc att gtt act ctg gaa acc aga gat ggg caa gtc ctg ggc			1035
456	Ile Leu Ile Ile Val Thr Leu Glu Thr Arg Asp Gly Gln Val Leu Gly			
457	285	290	295	
458	cga cgc tgc ttt gag gcc cgg atc tgc gct tgc cca gga aga gac agg			1083
459	Arg Arg Cys Phe Glu Ala Arg Ile Cys Ala Cys Pro Gly Arg Asp Arg			
460	300	305	310	
461	aag gcg gat gaa gat agc atc aga aag cag caa gtt tcc gac agt aca			1131
462	Lys Ala Asp Glu Asp Ser Ile Arg Lys Gln Gln Val Ser Asp Ser Thr			
463	315	320	325	
464	aag aac ggt gat ggt acg aag cgc ccg ttt cgt cag aac aca cat ggt			1179
465	Lys Asn Gly Asp Gly Thr Lys Arg Pro Phe Arg Gln Asn Thr His Gly			
466	330	335	340	345
467	atc cag atg aca tcc atc aag aaa cga aga tcc cca gat gat gaa ctg			1227
468	Ile Gln Met Thr Ser Ile Lys Lys Arg Arg Ser Pro Asp Asp Glu Leu			
469	350	355	360	
470	tta tac tta cca gtc agg ggc cgt gag act tat gaa atg ctg ttg aag			1275
471	Leu Tyr Leu Pro Val Arg Gly Arg Glu Thr Tyr Glu Met Leu Leu Lys			
472	365	370	375	

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473 atc aaa gag tcc ctg gaa ctc atg cag tac ctt cct cag cac aca att	1323
474 Ile Lys Glu Ser Leu Glu Leu Met Gln Tyr Leu Pro Gln His Thr Ile	
475 380 385 390	
476 gaa acg tac agg caa cag caa cag cag cag cac cac tta ctt cag	1371
E--> 477 395 400 405	amino acids
478 aaa cag acc tca ata cag tct cca tct tca tat ggt aac aac tcc cca	1419
479 Lys Gln Thr Ser Ile Gln Ser Pro Ser Ser Tyr Gly Asn Ser Ser Pro	
W--> 480 410 415 420 425	
481 cct ctg aac aaa atg aac aac atg aac aag ctg cct tct gtg aac cag	1467
482 Pro Leu Asn Lys Met Asn Ser Met Asn Lys Leu Pro Ser Val Ser Gln	
W--> 483 430 435 440	
484 ctt atc aac cct cag cag cgc aac gcc ctc act cct aca acc att cct	1515
485 Leu Ile Asn Pro Gln Gln Arg Asn Ala Leu Thr Pro Thr Thr Ile Pro	
W--> 486 445 450 455	
487 gat ggc atg gga gcc aac att ccc atg atg ggc acc cac atg cca atg	1563
488 Asp Gly Met Gly Ala Asn Ile Pro Met Met Gly Thr His Met Pro Met	
W--> 489 460 465 470	
490 gct gga gac atg aat gga ctc agc ccc acc cag gca ctc cct ccc cca	1611
491 Ala Gly Asp Met Asn Gly Leu Ser Pro Thr Gln Ala Leu Pro Pro Pro	
W--> 492 475 480 485	
493 ctc tcc atg cca tcc acc tcc cac tgc aca ccc cca cct ccg tat ccc	1659
494 Leu Ser Met Pro Ser Thr Ser His Cys Thr Pro Pro Pro Pro Tyr Pro	
W--> 495 490 495 500 505	
496 aca gat tgc agc att gtc agt ttc tta gcg agg ttg ggc tgt tca tca	1707
497 Thr Asp Cys Ser Ile Val Ser Phe Leu Ala Arg Leu Gly Cys Ser Ser	
W--> 498 510 515 520	
499 tgt ctg gac tat ttc acg acc cag ggg ctg acc acc atc tat cag att	1755
500 Cys Leu Asp Tyr Phe Thr Thr Gln Gly Leu Thr Thr Ile Tyr Gln Ile	
W--> 501 525 530 535	
502 gag cat tac tcc atg gat gat ctg gca agt ctg aaa atc cct gag caa	1803
503 Glu His Tyr Ser Met Asp Asp Leu Ala Ser Leu Lys Ile Pro Glu Gln	
W--> 504 540 545 550	
505 ttt cga cat gcg atc tgg aag ggc atc ctg gac cac cgg cag ctc cac	1851
506 Phe Arg His Ala Ile Trp Lys Gly Ile Leu Asp His Arg Gln Leu His	
W--> 507 555 560 565	
508 gaa ttc tcc tcc cct tct cat ctc ctg cgg acc cca agc agt gcc tct	1899
509 Glu Phe Ser Ser Pro Ser His Leu Leu Arg Thr Pro Ser Ser Ala Ser	
W--> 510 570 575 580 585	
511 aca gtc agt gtg ggc tcc agt gag acc cgg ggt gag cgt gtt att gat	1947
512 Thr Val Ser Val Gly Ser Ser Glu Thr Arg Gly Glu Arg Val Ile Asp	
W--> 513 590 595 600	
514 gct gtg cga ttc acc ctc cgc cag acc atc tct ttc cca ccc cga gat	1995
515 Ala Val Arg Phe Thr Leu Arg Gln Thr Ile Ser Phe Pro Pro Arg Asp	
W--> 516 605 610 615	
517 gag tgg aat gac ttc aac ttt gac atg gat gct cgc cgc aat aag caa	2043
518 Glu Trp Asn Asp Phe Asn Phe Asp Met Asp Ala Arg Arg Asn Lys Gln	
W--> 519 620 625 630	
520 cag cgc atc aaa gag gag ggg gag tgagcctcac catgtgagct cttcctatcc	2097
521 Gln Arg Ile Lys Glu Gly Glu	

RAW SEQUENCE LISTING

DATE: 03/29/2001

PATENT APPLICATION: US/09/670,568

TIME: 10:20:49

Input Set : A:\sequence listing (p99-16).txt  
Output Set: N:\CRF3\03292001\I670568.raw

W > 522 635 640  
523 ctctcctaac tgccagcccc ctaaaaggcac tcctgcttaa tcttcaaaggc cttctcccta 2157  
524 gtcctccccc ttccctcttgt ctgatttctt aggggaaggga gaagtaagag gctacctt 2217  
525 acctaacatc tgacctggca tctaattctg attctggctt taagccttca aaa 2270

VERIFICATION SUMMARY  
PATENT APPLICATION: US/09/670,568

DATE: 03/29/2001  
TIME: 10:20:50

Input Set : A:\sequence listing (p99-16).txt  
Output Set: N:\CRF3\03292001\I670568.raw

L:9 M:283 W: Missing Blank Line separator, <140> field identifier  
L:10 M:271 C: Current Filing Date differs, Replaced Current Filing Date  
L:30 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:1  
L:477 M:254 E: No. of Bases conflict, LENGTH:Input:405 Counted:1371 SEQ:5  
L:480 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5  
L:483 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5  
L:486 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5  
L:489 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5  
L:492 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5  
L:495 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5  
L:498 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5  
L:501 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5  
L:504 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5  
L:507 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5  
L:510 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5  
L:513 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5  
L:516 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5  
L:519 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5  
L:522 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5  
L:644 M:283 W: Missing Blank Line separator, <400> field identifier  
L:715 M:283 W: Missing Blank Line separator, <400> field identifier

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